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Sequence Listing was accepted.

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217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2008; month=10; day=29; hr=11; min=4; sec=37; ms=285;]

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Application No: 10562021 Version No: 3.0

Input Set:

Output Set:

Started: 2008-09-30 15:57:25.235
Finished: 2008-09-30 15:57:27.347
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 112 ms
Total Warnings: 9
Total Errors: 0
No. of SeqIDs Defined: 20
Actual SeqID Count: 20

Error code	Error Description
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W 402	Undefined organism found in <213> in SEQ ID (3)
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W 402	Undefined organism found in <213> in SEQ ID (6)
W 402	Undefined organism found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)

SEQUENCE LISTING

<110> Svendsen, Allan
 Beier, Lars
 Spendler, Tina
 Jensen, Morten Tovborg
 Jorgensen, Christel Thea

<120> CGTASE VARIANTS

<130> 10340-204-US

<140> 10562021

<141> 2006-01-11

<150> DK PCT/DK2004/000468

<151> 2004-07-01

<150> DK PA 2003 00994

<151> 2003-07-01

<150> US 60/484,004

<151> 2003-07-01

<160> 20

<170> PatentIn version 3.5

<210> 1

<211> 713

<212> PRT

<213> Bacillus agaradherens

<400> 1

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 20 25 30

Asn Ala Gln Gln Ala Thr Asp Arg Ser Asn Ser Val Asn Tyr Ser Thr
 35 40 45

Asp Gly Ile Tyr Gln Ile Val Thr Asp Arg Phe Tyr Asp Gly Asp Glu
 50 55 60

Ser Asn Asn Pro Ser Gly Glu Leu Tyr Ser Glu Gly Cys Lys Asn Leu
 65 70 75 80

Arg Lys Tyr Cys Gly Gly Asp Trp Gln Gly Ile Ile Asp Lys Ile Asp
 85 90 95

Asp Gly Tyr Leu Thr Asn Met Gly Val Thr Ala Leu Trp Ile Ser Pro
100 105 110

Pro Val Glu Asn Ile Phe Glu Thr Ile Asp Asp Glu Ser Gly Thr Thr
115 120 125

Ser Tyr His Gly Tyr Trp Ala Arg Asp Tyr Lys Lys Thr Asn Pro Phe
130 135 140

Phe Gly Ser Thr Glu Asp Phe Glu Arg Leu Ile Glu Thr Ala His Ser
145 150 155 160

His Asp Ile Lys Ile Val Ile Asp Leu Ala Pro Asn His Thr Ser Pro
165 170 175

Ala Asp Phe Asp Asn Pro Asn Tyr Ala Glu Asn Gly Ile Leu Tyr Asp
180 185 190

Asn Gly Asn Tyr Val Ser Ser Tyr Ser Asp Asn Ser Asp Leu Phe Leu
195 200 205

Tyr Asn Gly Gly Thr Asp Phe Ser Thr Tyr Glu Asp Glu Ile Tyr Arg
210 215 220

Asn Leu Phe Asp Leu Ala Ser Phe Asn His Ile Asn Ala Glu Leu Asn
225 230 235 240

Asn Tyr Leu Glu Asp Ala Val Lys Lys Trp Leu Asp Leu Gly Ile Asp
245 250 255

Gly Ile Arg Ile Asp Ala Val Ala His Met Pro Pro Gly Trp Gln Lys
260 265 270

Ala Tyr Met Asp Thr Ile Tyr Asp His Arg Ala Val Phe Thr Phe Gly
275 280 285

Glu Trp Phe Thr Gly Pro Tyr Gly Asn Glu Asp Tyr Thr Lys Phe Ala
290 295 300

Asn Asn Ser Gly Met Ser Val Leu Asp Phe Arg Phe Ala Gln Thr Thr
305 310 315 320

Arg	Asn	Val	Ile	Gly	Asn	Asn	Asn	Gly	Thr	Met	Tyr	Asp	Ile	Glu	Lys	325	330	335	
Met	Leu	Thr	Asp	Thr	Glu	Asn	Asp	Tyr	Asp	Arg	Pro	Gln	Asp	Gln	Val	340	345	350	
Thr	Phe	Leu	Asp	Asn	His	Asp	Met	Ser	Arg	Phe	Thr	Asn	Asp	Gly	Glu	355	360	365	
Ser	Thr	Arg	Thr	Thr	Asp	Ile	Gly	Leu	Ala	Leu	Met	Leu	Thr	Ser	Arg	370	375	380	
Gly	Val	Pro	Thr	Ile	Tyr	Tyr	Gly	Thr	Glu	Gln	Tyr	Met	Glu	Gly	Asp	385	390	395	400
Gly	Asp	Pro	Gly	Ser	Arg	Gly	Met	Met	Glu	Ser	Phe	Gly	Glu	Asn	Thr	405	410	415	
Asp	Ala	Tyr	Lys	Leu	Ile	Gln	Lys	Leu	Ala	Pro	Leu	Arg	Lys	Ser	Asn	420	425	430	
Pro	Ala	Tyr	Gly	Tyr	Gly	Thr	Thr	Lys	Glu	Arg	Trp	Ile	Asn	Asp	Asp	435	440	445	
Val	Ile	Ile	Tyr	Glu	Arg	Asn	Phe	Gly	Asp	Asn	Tyr	Ala	Leu	Ile	Ala	450	455	460	
Ile	Asn	Arg	Asn	Leu	Asn	Thr	Ser	Tyr	Asn	Ile	Gln	Gly	Leu	Gln	Thr	465	470	475	480
Glu	Met	Pro	Ser	Asn	Ser	Tyr	Asp	Asp	Val	Leu	Asp	Gly	Leu	Leu	Asp	485	490	495	
Gly	Gln	Ser	Ile	Val	Val	Asp	Asn	Asn	Gly	Glu	Val	Asn	Glu	Phe	Gln	500	505	510	
Met	Ser	Pro	Gly	Glu	Val	Gly	Val	Trp	Glu	Phe	Glu	Ala	Thr	Asn	Val	515	520	525	
Asp	Lys	Pro	Ser	Ile	Gly	Gln	Val	Gly	Pro	Ile	Ile	Gly	Glu	Ala	Gly	530	535	540	

Arg Thr Val Thr Ile Ser Gly Glu Gly Phe Gly Ser Ser Pro Gly Thr
545 550 555 560

Val Gln Phe Gly Ser Thr Ser Ala Glu Ile Val Ser Trp Asn Asp Thr
565 570 575

Val Ile Ile Ile Thr Val Pro Asn Asn Glu Ala Gly Tyr His Asp Ile
580 585 590

Thr Val Val Thr Glu Asp Glu Gln Val Ser Asn Ala Tyr Glu Phe Glu
595 600 605

Val Leu Thr Ala Asp Gln Val Thr Val Arg Phe Ile Ile Asp Asn Ala
610 615 620

Glu Thr Lys Met Gly Glu Asn Ile Phe Leu Val Gly Asn Val His Glu
625 630 635 640

Leu Gly Asn Trp Asp Pro Glu Gln Ser Val Gly Arg Phe Phe Asn Gln
645 650 655

Val Val Tyr Gln Tyr Pro Thr Trp Tyr Tyr Asp Val Asn Val Pro Ala
660 665 670

Asn Thr Asp Leu Glu Phe Lys Phe Ile Lys Ile Asp Gln Asp Asn Asn
675 680 685

Val Thr Trp Gln Ser Gly Ala Asn His Thr Tyr Ser Ser Pro Glu Ser
690 695 700

Gly Thr Gly Ile Ile Arg Val Asp Trp
705 710

<210> 2
<211> 713
<212> PRT
<213> Bacillus agaradherens

<400> 2

Met Arg Lys Lys Thr Leu Lys Arg Leu Leu Thr Leu Val Val Gly Leu
1 5 10 15

Val Ile Leu Ser Gly Leu Ser Ile Leu Asp Phe Ser Ile Thr Ser Ala
20 25 30

Ser Ala Gln Gln Ala Thr Asp Arg Ser Asn Ser Val Asn Tyr Ser Thr
35 40 45

Asp Val Ile Tyr Gln Ile Val Thr Asp Arg Phe Tyr Asp Gly Asp Glu
50 55 60

Ser Asn Asn Pro Ser Gly Glu Leu Tyr Ser Glu Asp Cys Lys Asn Leu
65 70 75 80

Arg Lys Tyr Cys Gly Gly Asp Trp Gln Gly Ile Ile Asp Lys Ile Asp
85 90 95

Asp Gly Tyr Leu Thr Asn Met Gly Val Thr Ala Leu Trp Ile Ser Pro
100 105 110

Pro Val Glu Asn Ile Phe Glu Thr Ile Asp Asp Glu Phe Gly Thr Thr
115 120 125

Ser Tyr His Gly Tyr Trp Ala Arg Asp Tyr Lys Lys Thr Asn Pro Phe
130 135 140

Phe Gly Ser Thr Glu Asp Phe Glu Arg Leu Ile Glu Thr Ala His Ser
145 150 155 160

His Asp Ile Lys Ile Val Ile Asp Leu Ala Pro Asn His Thr Ser Pro
165 170 175

Ala Asp Phe Asp Asn Pro Asp Tyr Ala Glu Asn Gly Val Leu Tyr Asp
180 185 190

Asp Gly Asn Tyr Leu Gly Ser Tyr Ser Asp Asp Ser Asp Leu Phe Leu
195 200 205

Tyr Asn Gly Gly Thr Asp Phe Ser Asn Tyr Glu Asp Glu Ile Tyr Arg
210 215 220

Asn Leu Phe Asp Leu Ala Ser Phe Asn His Ile Asn Ser Glu Leu Asn
225 230 235 240

Asn Tyr Leu Glu Asp Ala Val Lys Lys Trp Leu Asp Leu Gly Ile Asp
245 250 255

Gly Ile Arg Ile Asp Ala Val Ala His Met Pro Pro Gly Trp Lys Lys		
260	265	270
Ala Tyr Met Asp Thr Ile Tyr Asp His Arg Ala Val Phe Thr Phe Gly		
275	280	285
Glu Trp Phe Thr Gly Pro Ser Gly Asn Glu Asp Tyr Thr Lys Phe Ala		
290	295	300
Asn Asn Ser Gly Met Ser Val Leu Asp Phe Arg Phe Ala Gln Thr Thr		
305	310	315 320
Arg Asn Val Ile Gly Asn Asn Asn Gly Thr Met Tyr Asp Ile Glu Lys		
325	330	335
Met Leu Thr Asp Thr Glu Asn Asp Tyr Asp Arg Pro Gln Asp Gln Val		
340	345	350
Thr Phe Leu Asp Asn His Asp Met Ser Arg Phe Thr Asn Gly Gly Glu		
355	360	365
Ser Thr Arg Thr Thr Asp Ile Gly Leu Ala Leu Met Leu Thr Ser Arg		
370	375	380
Gly Val Pro Thr Ile Tyr Tyr Gly Thr Glu Gln Tyr Met Lys Gly Asp		
385	390	395 400
Gly Asp Pro Gly Ser Arg Gly Met Met Ala Ser Phe Asp Glu Asn Thr		
405	410	415
Asp Ala Tyr Lys Leu Ile Gln Lys Leu Ala Pro Leu Arg Lys Ser Asn		
420	425	430
Pro Ala Tyr Gly Tyr Gly Thr Thr Thr Glu Arg Trp Ile Asn Asp Asp		
435	440	445
Val Leu Ile Tyr Glu Arg His Phe Gly Glu Asn Tyr Ala Leu Ile Ala		
450	455	460
Ile Asn Arg Ser Leu Asn Thr Ser Tyr Asn Ile Gln Gly Leu Gln Thr		
465	470	475 480

Glu Met Pro Ser Asn Ser Tyr Asp Asp Val Leu Asp Gly Leu Leu Asp
485 490 495

Gly Gln Ser Ile Val Val Asp Asn Lys Gly Gly Val Asn Glu Phe Gln
500 505 510

Met Ser Pro Gly Glu Val Ser Val Trp Glu Phe Glu Ala Glu Asn Val
515 520 525

Asp Lys Pro Ser Ile Gly Gln Val Gly Pro Ile Ile Gly Glu Ala Gly
530 535 540

Arg Thr Val Thr Ile Ser Gly Glu Gly Phe Gly Ser Ser Gln Gly Thr
545 550 555 560

Val His Phe Gly Ser Thr Ser Ala Glu Ile Leu Ser Trp Asn Asp Thr
565 570 575

Ile Ile Thr Leu Thr Val Pro Asn Asn Glu Ala Gly Tyr His Asp Ile
580 585 590

Thr Val Val Thr Glu Asp Glu Gln Val Ser Asn Ala Tyr Glu Phe Glu
595 600 605

Val Leu Thr Ala Asp Gln Val Thr Val Arg Phe Ile Ile Asp Asn Ala
610 615 620

Glu Thr Lys Leu Gly Glu Asn Val Phe Leu Val Gly Asn Val His Glu
625 630 635 640

Leu Gly Asn Trp Asp Pro Glu Gln Ser Val Gly Arg Phe Phe Asn Gln
645 650 655

Ile Val Tyr Gln Tyr Pro Thr Trp Tyr Tyr Asp Val Asn Val Pro Ala
660 665 670

Asn Thr Asp Leu Glu Phe Lys Phe Ile Lys Ile Asp Gln Asp Asn Asn
675 680 685

Val Ile Trp Gln Ser Gly Ala Asn Gln Thr Tyr Ser Ser Pro Glu Ser
690 700

Gly Thr Gly Ile Ile Arg Val Asp Trp

705 710

<210> 3

<211> 714

<212> PRT

<213> Panibacillus macerans

<400> 3

Met Lys Ser Arg Tyr Lys Arg Leu Thr Ser Leu Ala Leu Ser Leu Ser
1 5 10 15

Met Ala Leu Gly Ile Ser Leu Pro Ala Trp Ala Ser Pro Asp Thr Ser
20 25 30

Val Asp Asn Lys Val Asn Phe Ser Thr Asp Val Ile Tyr Gln Ile Val
35 40 45

Thr Asp Arg Phe Ala Asp Gly Asp Arg Thr Asn Asn Pro Ala Gly Asp
50 55 60

Ala Phe Ser Gly Asp Arg Ser Asn Leu Lys Leu Tyr Phe Gly Gly Asp
65 70 75 80

Trp Gln Gly Ile Ile Asp Lys Ile Asn Asp Gly Tyr Leu Thr Gly Met
85 90 95

Gly Val Thr Ala Leu Trp Ile Ser Gln Pro Val Glu Asn Ile Thr Ser
100 105 110

Val Ile Lys Tyr Ser Gly Val Asn Asn Thr Ser Tyr His Gly Tyr Trp
115 120 125

Ala Arg Asp Phe Lys Gln Thr Asn Asp Ala Phe Gly Asp Phe Ala Asp
130 135 140

Phe Gln Asn Leu Ile Asp Thr Ala His Ala His Asn Ile Lys Val Val
145 150 155 160

Ile Asp Phe Ala Pro Asn His Thr Ser Pro Ala Asp Arg Asp Asn Pro
165 170 175

Gly Phe Ala Glu Asn Gly Gly Met Tyr Asp Asn Gly Ser Leu Leu Gly
180 185 190

Ala Tyr Ser Asn Asp Thr Ala Gly Leu Phe His His Asn Gly Gly Thr
 195 200 205

Asp Phe Ser Thr Ile Glu Asp Gly Ile Tyr Lys Asn Leu Tyr Asp Leu
 210 215 220

Ala Asp Ile Asn His Asn Asn Asn Ala Met Asp Ala Tyr Phe Lys Ser
 225 230 235 240

Ala Ile Asp Leu Trp Leu Gly Met Gly Val Asp Gly Ile Arg Phe Asp
 245 250 255

Ala Val Lys His Met Pro Phe Gly Trp Gln Lys Ser Phe Val Ser Ser
 260 265 270

Ile Tyr Gly Gly Asp His Pro Val Phe Thr Phe Gly Glu Trp Tyr Leu
 275 280 285

Gly Ala Asp Gln Thr Asp Gly Asp Asn Ile Lys Phe Ala Asn Glu Ser
 290 295 300

Gly Met Asn Leu Leu Asp Phe Glu Tyr Ala Gln Glu Val Arg Glu Val
 305 310 315 320

Phe Arg Asp Lys Thr Glu Thr Met Lys Asp Leu Tyr Glu Val Leu Ala
 325 330 335

Ser Thr Glu Ser Gln Tyr Asp Tyr Ile Asn Asn Met Val Thr Phe Ile
 340 345 350

Asp Asn His Asp Met Asp Arg Phe Gln Val Ala Gly Ser Gly Thr Arg
 355 360 365

Ala Thr Glu Gln Ala Leu Ala Leu Thr Leu Thr Ser Arg Gly Val Pro
 370 375 380

Ala Ile Tyr Tyr Gly Thr Glu Gln Tyr Met Thr Gly Asp Gly Asp Pro
 385 390 395 400

Asn Asn Arg Ala Met Met Thr Ser Phe Asn Thr Gly Thr Thr Ala Tyr
 405 410 415

Lys Val Ile Gln Ala Leu Ala Pro Leu Arg Lys Ser Asn Pro Ala Ile
 420 425 430

Ala Tyr Gly Thr Thr Thr Glu Arg Trp Val Asn Asn Asp Val Leu Ile
 435 440 445

Ile Glu Arg Lys Phe Gly Ser Ser Ala Ala Leu Val Ala Ile Asn Arg
 450 455 460

Asn Ser Ser Ala Ala Tyr Pro Ile Ser Gly Leu Leu Ser Ser Leu Pro
 465 470 475 480

Ala Gly Thr Tyr Ser Asp Val Leu Asn Gly Leu Leu Asn Gly Asn Ser
 485 490 495

Ile Thr Val Gly Ser Gly Gly Ala Val Thr Asn Phe Thr Leu Ala Ala
 500 505 510

Gly Gly Thr Ala Val Trp Gln Tyr Thr Ala Pro Glu Thr Ser Pro Ala
 515 520 525

Ile Gly Asn Val Gly Pro Thr Met Gly Gln Pro Gly Asn Ile Val Thr
 530 535 540

Ile Asp Gly Arg Gly Phe Gly Gly Thr Ala Gly Thr Val Tyr Phe Gly
 545 550 555 560

Thr Thr Ala Val Thr Gly Ser Gly Ile Val Ser Trp Glu Asp Thr Gln
 565 570 575

Ile Lys Ala Val Ile Pro Lys Val Ala Ala Gly Lys Thr Gly Val Ser
 580 585 590

Val Lys Thr Se